Examiner relies on disclosure at col. 5, lines 53-58, col. 5, lines 58-60, Fig. 10, and claim 28, particularly, col. 164, lines 38-46 and 46-42. This rejection is respectfully traversed.

Closer inspection of each of the above passages from the cited reference indicates steps (e)-(h) of present claim 1 are not present. Specifically, step (e) of claim 1 requires providing a further array of probes based on an estimate of a target sequence resulting from a prior hybridization, step (f) requires hybridizing the target nucleic acid to the further array of probes, step (g) requires determining relative hybridization of the target to the probes in the further array, and step (h) requires reestimating the sequence of the target nucleic acid

The passages cited by the Examiner will be examined in reverse order. Claim 28 recites general methods for analyzing a target nucleic acid using four sets of probes containing corresponding probes differing from each other at an interrogation position. The methods are further discussed e.g., cols. 10-19 of the Cronin patent. In these methods, each base of interest in a target nucleic acid is determined by a comparison of four corresponding probes. The final step (d) of the claim indicates that additional corresponding probes are compared until each base of interest in the target sequence is determined. Effectively, this step is specifying additional analyses of the same hybridization pattern with each analysis providing the identity of one further base in a target sequence. However, step (d) of claim 28 of the Cronin patent does not specify that a further array of probes is produced, much less a further array based on a previously estimated target sequence. Step (d) of claim 28 also does not specify a second hybridization is performed involving the further array. Perforce, claim 28 of Cronin is also silent as to determining the relative hybridization of probes in the second hybridization and reestimating the sequence of a target nucleic acid. It is reiterated that step (d) of claim 28 refers merely to additional analyses performed on the same hybridization pattern to determine the identity of multiple bases in the target sequence.

Col. 5, lines 53-58 and 58-60 and Fig. 10 of Cronin relate to an elaboration of the method of claim 28 of the Cronin patent in which two target nucleic acids can be analyzed independently of each other. The method is discussed in more detail in the paragraph bridging cols. 15-16 of Cronin. In this method, an array is designed to include probes tiling two different target nucleic acids, and the analysis of each proceeds essentially independently of each other. The method is particularly useful for analyzing heterozygous alleles of a gene (see

col. 5, lines 60-61). Present claim 1 differs from the above disclosure, for example, in that the further array in claim 1 is not designed to be complementary to a second target nucleic acid, but rather to an estimate of the sequence of the first target nucleic acid. Thus, in the presently claimed methods, the same target nucleic acid is hybridized to two (or more) arrays designed based on different estimates of the target sequence, whereas in Cronin two different target nucleic acids are hybridized to the same array. Further, in present claim 1, the estimated and reestimated sequences in present claim 1, represent two estimates (usually of increasing accuracy) of the same target nucleic acid, whereas the method of Cronin results in a single analysis of each of two different target nucleic acids.

For these reasons, it is submitted that the presently claimed invention is distinguished over Cronin.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,

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